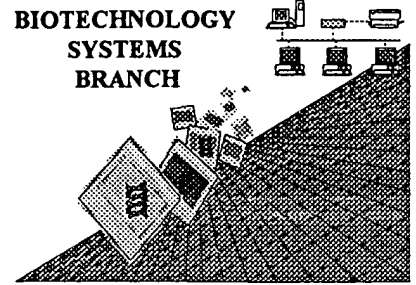


# **RAW SEQUENCE LISTING** **ERROR REPORT**

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: 09/358,321  
Art Unit / Team No. : 01PE  
Date Processed by STIC: 7/30/99

**THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.**

**PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,**
- 2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY**

**THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.**

**IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:**

**MARK SPENCER 703-308-4212**

# Raw Sequence Listing Error Summary

## ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/358,321

**ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE**

- 1        Wrapped Nucleics      The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2        Wrapped Aminos      The amino acid number/text at the end of each line "wrapped " down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3        Incorrect Line Length      The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4        Misaligned Amino Acid      The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs  
Numbering      between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5        Non-ASCII      This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6        Variable Length      Sequence(s)        contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and  
indicate in the (ix) feature section that some may be missing.
- 7        PatentIn ver. 2.0 "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid  
sequence(s)       . Normally, PatentIn would automatically generate this section from the  
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section  
to the subsequent amino acid sequence.
- 8        Skipped Sequences      Sequence(s)        missing. If intentional, please use the following format for each skipped sequence:  
(OLD RULES)      (2) INFORMATION FOR SEQ ID NO:X:  
                         (i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")  
                         (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:  
                         This sequence is intentionally skipped  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9        Skipped Sequences      Sequence(s)        missing. If intentional, please use the following format for each skipped sequence.  
(NEW RULES)      <210> sequence id number  
                         <400> sequence id number  
                         000
- 10        Use of n's or Xaa's      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
(NEW RULES)      Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11        Use of <213>Organism      Sequence(s)        are missing this mandatory field or its response.  
(NEW RULES)
- 12        Use of <220>Feature      Sequence(s)        are missing the <220>Feature and associated headings.  
(NEW RULES)      Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"  
Please explain source of genetic material in <220> t <223> section.  
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13        PatentIn ver. 2.0 "bug"      Please do not use "Copy to Disk" function of PatentIn versl n 2.0. This causes a corrupted  
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).  
Instead, please use "File Manager" or any other means to copy file to floppy disk.  
AKS-Biotechnology Systems Branch- 5/15/99

PAGE: 1

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/358,321

DATE: 07/30/1999  
TIME: 11:51:11

Input Set: I358321.RAW

This Raw Listing contains the General Information  
Section and up to first 5 pages.

*see  
p. 5, too*

Does Not Comply  
Corrected Diskette Needed

1 <110> APPLICANT: Sukhapinda, Kitisri  
2 Hasler, James M  
3 Petell, James K  
4 Strickland, James A  
5 Folkerts, Otto  
6 <120> TITLE OF INVENTION: ANTIBODY-MEDIATED DOWN-REGULATION OF PLANT PROTEINS  
7 <130> FILE REFERENCE: 50447  
8 <140> CURRENT APPLICATION NUMBER: US/09/358,321  
9 <141> CURRENT FILING DATE: 1999-07-21  
10 <150> EARLIER APPLICATION NUMBER: US 60/093,587  
11 <151> EARLIER FILING DATE: 1998-07-21  
12 <160> NUMBER OF SEQ ID NOS: 56  
13 <170> SOFTWARE: PatentIn Ver. 2.0  
14 <210> SEQ ID NO 1  
15 <211> LENGTH: 17  
16 <212> TYPE: DNA  
17 <213> ORGANISM: Artificial Sequence  
18 <220> FEATURE:  
19 <223> OTHER INFORMATION: Description of Artificial Sequence:5' primer  
20 <400> SEQUENCE: 1  
W--> 21 gargaraaym gncaygg 17  
22 <210> SEQ ID NO 2  
23 <211> LENGTH: 18  
24 <212> TYPE: DNA  
25 <213> ORGANISM: Artificial Sequence  
26 <220> FEATURE:  
27 <223> OTHER INFORMATION: Description of Artificial Sequence:3' primer  
28 <400> SEQUENCE: 2  
W--> 29 ytcrtgcky tttcrtc 18  
30 <210> SEQ ID NO 3  
31 <211> LENGTH: 276  
32 <212> TYPE: DNA  
33 <213> ORGANISM: Zea mays  
34 <220> FEATURE:  
35 <221> NAME/KEY: CDS  
36 <222> LOCATION: (1)..(276)  
37 <400> SEQUENCE: 3  
38 gag gag aac agg cat ggt gat ctg ctc aac aag tat atg tac ctc act 48  
39 Glu Glu Asn Arg His Gly Asp Leu Leu Asn Lys Tyr Met Tyr Leu Thr  
40 1 5 10 15  
41 ggg agg gtg gat atg agg cag att gag aag aca att cag tat ctt att 96  
42 Gly Arg Val Asp Met Arg Gln Ile Glu Lys Thr Ile Gln Tyr Leu Ile  
43 20 25 30  
44 ggc tct gga atg gat cct agg act gag aat aat cct tat ctt ggt ttc 144

PAGE: 2

**RAW SEQUENCE LISTING**  
**PATENT APPLICATION US/09/358,321**

 DATE: 07/30/1999  
 TIME: 11:51:11

Input Set: I358321.RAW

```

45      Gly Ser Gly Met Asp Pro Arg Thr Glu Asn Asn Pro Tyr Leu Gly Phe
46              35              40              45
47      atc tac acc tcc ttc caa gag cgg gcg acc ttc atc tca cac ggg aac      192
48      Ile Tyr Thr Ser Phe Gln Glu Arg Ala Thr Phe Ile Ser His Gly Asn
49              50              55              60
50      act gct cgt cac gcc aag gac ttt ggc gac tta aag ctt gca caa atc      240
51      Thr Ala Arg His Ala Lys Asp Phe Gly Asp Leu Lys Leu Ala Gln Ile
52              65              70              75              80
53      tgc ggc atc atc gcc tca gat gag aag cga cat gaa      276
54      Cys Gly Ile Ile Ala Ser Asp Glu Lys Arg His Glu
55              85              90
56      <210> SEQ ID NO 4
57      <211> LENGTH: 92
58      <212> TYPE: PRT
59      <213> ORGANISM: Zea mays
60      <400> SEQUENCE: 4
61      Glu Glu Asn Arg His Gly Asp Leu Leu Asn Lys Tyr Met Tyr Leu Thr
62              1              5              10              15
63      Gly Arg Val Asp Met Arg Gln Ile Glu Lys Thr Ile Gln Tyr Leu Ile
64              20              25              30
65      Gly Ser Gly Met Asp Pro Arg Thr Glu Asn Asn Pro Tyr Leu Gly Phe
66              35              40              45
67      Ile Tyr Thr Ser Phe Gln Glu Arg Ala Thr Phe Ile Ser His Gly Asn
68              50              55              60
69      Thr Ala Arg His Ala Lys Asp Phe Gly Asp Leu Lys Leu Ala Gln Ile
70              65              70              75              80
71      Cys Gly Ile Ile Ala Ser Asp Glu Lys Arg His Glu
72              85              90
73      <210> SEQ ID NO 5
74      <211> LENGTH: 1621
75      <212> TYPE: DNA
76      <213> ORGANISM: Zea mays
77      <220> FEATURE:
78      <221> NAME/KEY: CDS
79      <222> LOCATION: (146)..(1324)
80      <220> FEATURE:
81      <221> NAME/KEY: mat_peptide
82      <222> LOCATION: (239)..(1324)
83      <400> SEQUENCE: 5
84      cgcacgcgcc ctctgccgct tgttcggtcc tcgcgctcgc caccaggcac caccacacac 60
85      atcccaatct cgcgagggca agcagcaggg tctgcggcgg cggcggcggc cgcgcttccg 120
86      gctcccccttc ccattggcct ccacg atg gcg ctc cgc ctc aac gac gtc gcg      172
87              Met Ala Leu Arg Leu Asn Asp Val Ala
88              -30              -25
89      ctc tgc ctc tcc ccg ccg ctc gcc gcc cgc cgc cgc cgc cgc agc agc      220
90      Leu Cys Leu Ser Pro Pro Leu Ala Ala Arg Arg Arg Arg Arg Ser Ser
91              -20              -15              -10
92      ggc agg ttc gtc gcc gtc gcc tcc atg acg tcc gcc gtc tcc acc aag      268
93      Gly Arg Phe Val Ala Val Ala Ser Met Thr Ser Ala Val Ser Thr Lys
94              -5              -1      1              5              10

```

PAGE: 3

**RAW SEQUENCE LISTING**  
**PATENT APPLICATION US/09/358,321**

 DATE: 07/30/1999  
 TIME: 11:51:11

Input Set: I358321.RAW

|     |   |      |
|-----|---|------|
| 95  | gtc gag aat aag aag cca ttt gct cct cca agg gag gta cat gtc cag | 316  |
| 96  | Val Glu Asn Lys Lys Pro Phe Ala Pro Pro Arg Glu Val His Val Gln |      |
| 97  | 15 20 25  |      |
| 98  | gtt aca cat tca atg cca cct cac aag att gaa att ttc aag tcg ctt | 364  |
| 99  | Val Thr His Ser Met Pro Pro His Lys Ile Glu Ile Phe Lys Ser Leu |      |
| 100 | 30 35 40  |      |
| 101 | gat gat tgg gct aga gat aat atc ttg acg cat ctc aag cca gtc gag | 412  |
| 102 | Asp Asp Trp Ala Arg Asp Asn Ile Leu Thr His Leu Lys Pro Val Glu |      |
| 103 | 45 50 55  |      |
| 104 | aag tgt tgg cag cca cag gat ttc ctc ccg gac cca gca tct gaa gga | 460  |
| 105 | Lys Cys Trp Gln Pro Gln Asp Phe Leu Pro Asp Pro Ala Ser Glu Gly |      |
| 106 | 60 65 70  |      |
| 107 | ttt cat gat gaa gtt aag gag ctc aga gaa cgt gcc aag gaa atc cct | 508  |
| 108 | Phe His Asp Glu Val Lys Glu Leu Arg Glu Arg Ala Lys Glu Ile Pro |      |
| 109 | 75 80 85 90   |      |
| 110 | gat gat tat ttt gtt tgt ttg gtg gga gac atg att acc gag gaa gct | 556  |
| 111 | Asp Asp Tyr Phe Val Cys Leu Val Gly Asp Met Ile Thr Glu Glu Ala |      |
| 112 | 95 100 105  |      |
| 113 | cta cca aca tac cag act atg ctt aac acc ctc gac ggt gtc aga gat | 604  |
| 114 | Leu Pro Thr Tyr Gln Thr Met Leu Asn Thr Leu Asp Gly Val Arg Asp |      |
| 115 | 110 115 120   |      |
| 116 | gag aca ggt gca agc ccc act gcc tgg gct gtt tgg acg agg gca tgg | 652  |
| 117 | Glu Thr Gly Ala Ser Pro Thr Ala Trp Ala Val Trp Thr Arg Ala Trp |      |
| 118 | 125 130 135   |      |
| 119 | act gct gag gag aac agg cat ggt gat ctg ctc aac aag tat atg tac | 700  |
| 120 | Thr Ala Glu Glu Asn Arg His Gly Asp Leu Leu Asn Lys Tyr Met Tyr |      |
| 121 | 140 145 150   |      |
| 122 | ctc act ggg agg gtg gat atg agg cag att gag aag aca att cag tat | 748  |
| 123 | Leu Thr Gly Arg Val Asp Met Arg Gln Ile Glu Lys Thr Ile Gln Tyr |      |
| 124 | 155 160 165 170   |      |
| 125 | ctt att ggc tct gga atg gat cct agg act gag aat aat cct tat ctt | 796  |
| 126 | Leu Ile Gly Ser Gly Met Asp Pro Arg Thr Glu Asn Asn Pro Tyr Leu |      |
| 127 | 175 180 185   |      |
| 128 | ggt ttc atc tac acc tcc ttc caa gag cgg gcg acc ttc atc tca cac | 844  |
| 129 | Gly Phe Ile Tyr Thr Ser Phe Gln Glu Arg Ala Thr Phe Ile Ser His |      |
| 130 | 190 195 200   |      |
| 131 | ggg aac act gct cgt cac gcc aag gac ttt ggc gac tta aag ctt gca | 892  |
| 132 | Gly Asn Thr Ala Arg His Ala Lys Asp Phe Gly Asp Leu Lys Leu Ala |      |
| 133 | 205 210 215   |      |
| 134 | caa atc tgc ggc atc atc gcc tca gat gag aag cga cat gaa act gcg | 940  |
| 135 | Gln Ile Cys Gly Ile Ile Ala Ser Asp Glu Lys Arg His Glu Thr Ala |      |
| 136 | 220 225 230   |      |
| 137 | tac acc aag atc gtg gag aag ctg ttt gag atc gac cct gat ggt acc | 988  |
| 138 | Tyr Thr Lys Ile Val Glu Lys Leu Phe Glu Ile Asp Pro Asp Gly Thr |      |
| 139 | 235 240 245 250   |      |
| 140 | gtg gtc gct ctg gct gac atg atg agg aag aag atc tca atg cct gcc | 1036 |
| 141 | Val Val Ala Leu Ala Asp Met Met Arg Lys Lys Ile Ser Met Pro Ala |      |
| 142 | 255 260 265   |      |
| 143 | cac ctg atg ttt gac ggg cag gac gac aag ctg ttc gag cac ttc tcc | 1084 |
| 144 | His Leu Met Phe Asp Gly Gln Asp Asp Lys Leu Phe Glu His Phe Ser |      |

PAGE: 4

# RAW SEQUENCE LISTING PATENT APPLICATION US/09/358,321

DATE: 07/30/1999  
TIME: 11:51:11

Input Set: I358321.RAW

```

145          270          275          280
146  atg gtc gcg cag agg ctt ggc gtt tac acc gcc agg gac tac gcc gac 1132
147  Met Val Ala Gln Arg Leu Gly Val Tyr Thr Ala Arg Asp Tyr Ala Asp
148          285          290          295
149  atc ctc gag ttc ctc gtc gac agg tgg aag gtg gcg agc ctg act ggt 1180
150  Ile Leu Glu Phe Leu Val Asp Arg Trp Lys Val Ala Ser Leu Thr Gly
151          300          305          310
152  ctg tcg ggt gaa ggg aac aag gcg cag gac tac ctt tgc acc ctt gct 1228
153  Leu Ser Gly Glu Gly Asn Lys Ala Gln Asp Tyr Leu Cys Thr Leu Ala
154  315          320          325          330
155  tca aga atc agg agg ctg gag gag agg gcc cag agc aga gcc aag aaa 1276
156  Ser Arg Ile Arg Arg Leu Glu Glu Arg Ala Gln Ser Arg Ala Lys Lys
157          335          340          345
158  gcc ggc acg ctg cct ttc agc tgg gta tac ggt agg gac gtc caa ctg 1324
159  Ala Gly Thr Leu Pro Phe Ser Trp Val Tyr Gly Arg Asp Val Gln Leu
160          350          355          360
161  tgagatcgga aacctgctgc ggactgctta gacaagacct gctgtgtctg cgttacatag 1384
162  gtctccaggt tttgatcaaa tgggtcccggtg tcgtcttata gagcgatagg agaactgtgt 1444
163  ggtctgtggt gtagctttgt ttttattttg tatttttctg ctttgatgta caacctgtgg 1504
164  ccgcatgaac tggggcggtg agatgggagc gaccatgccg tactttgtct gtcgctggcg 1564
165  gtgtgtttcg gtatgttatt tgagttgctc agatctgtta aaaaaaaaaa aaaaaaa 1621
166 <210> SEQ ID NO 6
167 <211> LENGTH: 393
168 <212> TYPE: PRT
169 <213> ORGANISM: Zea mays
170 <400> SEQUENCE: 6
171  Met Ala Leu Arg Leu Asn Asp Val Ala Leu Cys Leu Ser Pro Pro Leu
172  -30          -25          -20
173  Ala Ala Arg Arg Arg Arg Arg Ser Ser Gly Arg Phe Val Ala Val Ala
174  -15          -10          -5          -1 1
175  Ser Met Thr Ser Ala Val Ser Thr Lys Val Glu Asn Lys Lys Pro Phe
176  5          10          15
177  Ala Pro Pro Arg Glu Val His Val Gln Val Thr His Ser Met Pro Pro
178  20          25          30
179  His Lys Ile Glu Ile Phe Lys Ser Leu Asp Asp Trp Ala Arg Asp Asn
180  35          40          45
181  Ile Leu Thr His Leu Lys Pro Val Glu Lys Cys Trp Gln Pro Gln Asp
182  50          55          60          65
183  Phe Leu Pro Asp Pro Ala Ser Glu Gly Phe His Asp Glu Val Lys Glu
184  70          75          80
185  Leu Arg Glu Arg Ala Lys Glu Ile Pro Asp Asp Tyr Phe Val Cys Leu
186  85          90          95
187  Val Gly Asp Met Ile Thr Glu Glu Ala Leu Pro Thr Tyr Gln Thr Met
188  100          105          110
189  Leu Asn Thr Leu Asp Gly Val Arg Asp Glu Thr Gly Ala Ser Pro Thr
190  115          120          125
191  Ala Trp Ala Val Trp Thr Arg Ala Trp Thr Ala Glu Glu Asn Arg His
192  130          135          140          145
193  Gly Asp Leu Leu Asn Lys Tyr Met Tyr Leu Thr Gly Arg Val Asp Met
194          150          155          160

```

PAGE: 5

# RAW SEQUENCE LISTING PATENT APPLICATION US/09/358,321

DATE: 07/30/1999  
TIME: 11:51:11

Input Set: I358321.RAW

```

195      Arg Gln Ile Glu Lys Thr Ile Gln Tyr Leu Ile Gly Ser Gly Met Asp
196                      165                      170                      175
197      Pro Arg Thr Glu Asn Asn Pro Tyr Leu Gly Phe Ile Tyr Thr Ser Phe
198                      180                      185                      190
199      Gln Glu Arg Ala Thr Phe Ile Ser His Gly Asn Thr Ala Arg His Ala
200                      195                      200                      205
201      Lys Asp Phe Gly Asp Leu Lys Leu Ala Gln Ile Cys Gly Ile Ile Ala
202      210                      215                      220                      225
203      Ser Asp Glu Lys Arg His Glu Thr Ala Tyr Thr Lys Ile Val Glu Lys
204                      230                      235                      240
205      Leu Phe Glu Ile Asp Pro Asp Gly Thr Val Val Ala Leu Ala Asp Met
206                      245                      250                      255
207      Met Arg Lys Lys Ile Ser Met Pro Ala His Leu Met Phe Asp Gly Gln
208                      260                      265                      270
209      Asp Asp Lys Leu Phe Glu His Phe Ser Met Val Ala Gln Arg Leu Gly
210                      275                      280                      285
211      Val Tyr Thr Ala Arg Asp Tyr Ala Asp Ile Leu Glu Phe Leu Val Asp
212      290                      295                      300                      305
213      Arg Trp Lys Val Ala Ser Leu Thr Gly Leu Ser Gly Glu Gly Asn Lys
214                      310                      315                      320
215      Ala Gln Asp Tyr Leu Cys Thr Leu Ala Ser Arg Ile Arg Arg Leu Glu
216                      325                      330                      335
217      Glu Arg Ala Gln Ser Arg Ala Lys Lys Ala Gly Thr Leu Pro Phe Ser
218                      340                      345                      350
219      Trp Val Tyr Gly Arg Asp Val Gln Leu
220                      355                      360

```

221 &lt;210&gt; SEQ ID NO 7

222 &lt;211&gt; LENGTH: 30

223 &lt;212&gt; TYPE: DNA

224 &lt;213&gt; ORGANISM: Artificial Sequence

225 &lt;220&gt; FEATURE:

226 &lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence:primer

227 &lt;400&gt; SEQUENCE: 7

228 atggctagcc tccgcctcaa cgacgtcgcg

30

229 &lt;210&gt; SEQ ID NO 8

230 &lt;211&gt; LENGTH: 36

231 &lt;212&gt; TYPE: DNA

232 &lt;213&gt; ORGANISM: Artificial Sequence

233 &lt;220&gt; FEATURE:

234 &lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence:primer

235 &lt;400&gt; SEQUENCE: 8

236 aaagctagct catcacagtt ggacgtccct accgta

36

237 &lt;210&gt; SEQ ID NO 9

238 &lt;211&gt; LENGTH: 30

239 &lt;212&gt; TYPE: DNA

240 &lt;213&gt; ORGANISM: Artificial Sequence

241 &lt;220&gt; FEATURE:

242 &lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence:primer

243 &lt;400&gt; SEQUENCE: 9

244 accatggcta gcatgaagtc cgccgtctcc

30

## Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Input Set: I358321.RAW

| Line | ? Error/Warning                       | Original Text                             |
|------|---------------------------------------|---|
| 21   | W "N" or "Xaa" used: Feature required | gargaraaym gncaygg                        |
| 29   | W "N" or "Xaa" used: Feature required | ytcrtnckky ttytcrtc                       |
| 393  | W "N" or "Xaa" used: Feature required | Glu Val His Val Gln Val Thr Xaa Ser Met   |
| 453  | W "N" or "Xaa" used: Feature required | accctcctcc tggtcnnnnn ntcagntgtc ancagt g |